



SEQUENCE LISTING

<110> Yoshida, Roberta
Kootstra, Anna

<120> Phenylalanine Ammonia Lyase Polypeptide and
Polynucleotide Sequences and Methods of Obtaining and
Using Same

<130> 29479/500NSCA

<140> US 09/939,408

<141> 2001-08-24

<150> US 09/624,693

<151> 2000-07-24

<150> PCT/US01/23270

<151> 2001-07-24

<160> 30

<170> PatentIn Ver. 2.0

<210> 1

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic
primer OLI 61

<400> 1

gacggatcca ctatggcbcc btcsgtsgac tcgat

35

<210> 2

<211> 33

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<213> Artificial Sequence

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<221> modified_base
<222> (13)
<223> n = (a or c or g or t/u) or (unknown or other)
<223> Description of Artificial Sequence: Synthetic
Primer OLI 63

<400> 2
gacgaattct tangccatca tcttsacsag gac

33

<210> 3
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<222> (24, 25, 29, 30, 34, 35)
<223> n = i or inosine
<223> Description of Artificial Sequence: Synthetic
Primer AAP

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ggccacgcgt cgactagtagt gggnnngggnn gggnnng

36

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<211> 33
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Primer GSP2

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cgcgattca gaatgcctc gtcgtccttg acc

33

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<223> Description of Artificial Sequence: Synthetic
Primer AUAP

<400> 5

ggccacgcgt cgactagtac

20

<210> 6

<211> 33

<212> DNA

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<223> Description of Artificial Sequence: Synthetic
Primer GSP4

<400> 6

ccggaattcc gacgagccgg aaaggagcgt gcg

33

<210> 7

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer AP

<400> 7

ggccacgcgt cgactagtac tttttttttt tttttttt

37

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer GSP5

<400> 8

ggccaaggac gacgaggga ttct

24

<210> 9

<211> 38

<212> DNA

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<223> Description of Artificial Sequence: Synthetic
Primer GSP6

<400> 9

ccgggatcca tgatgcacgc ctactcgact ctctcgct

38

<210> 10

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 77

<400> 10

atcgaattcc actctaaccg gtcactagca ctccg

36

<210> 11

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 78

<400> 11

atcggtatccc acgacacgac gtcgaaaagc tgggtct

36

<210> 12
 <211> 2419
 <212> DNA
 <213> Rhodotorula graminis

<220>
 <221> CDS
 <222> (37)..(2196)

,<220>
 <221> modified_base
 <222> (494)
 <223> Other information: y = t or c

<220>
 <221> unsure
 <222> (493)..(495)
 <223> Other information: Xaa = Val or Ala

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 1 5
 tcg ctc gcc acc acg ctc gcc aac ggc ttt acc aac ggc tcg cac gcc 102
 Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe Thr Asn Gly Ser His Ala
 10 15 20
 gct ccg acc aag tcg gct gcg ggc ccc act tcg gct ctc cgc cgc acg 150
 Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr Ser Ala Leu Arg Arg Thr
 25 30 35
 ccc ggc ctc gat ggc cac gcc gcg cac cag tcg cag ctc gag atc gtg 198
 Pro Gly Leu Asp Gly His Ala Ala His Gln Ser Gln Leu Glu Ile Val
 40 45 50

cag gag ctc ctc agc gac ccc acc gac gac gtc gtc gag ctc agc ggg	246
Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp Val Val Glu Leu Ser Gly	
55 60 65 70	
tac agc ctc acc gtc cgt gac gtt gtc ggc gcc gcc cgc aag ggg cgc	294
Tyr Ser Leu Thr Val Arg Asp Val Val Gly Ala Ala Arg Lys Gly Arg	
75 80 85	
agg gtc cgc gtc cag aac gac gac gag atc cgc gca cgc gtc gac aag	342
Arg Val Arg Val Gln Asn Asp Asp Glu Ile Arg Ala Arg Val Asp Lys	
90 95 100	
agc gtc gac ttc ctc aag gcc cag ctt cag aac tcg gtc tac gga gtc	390
Ser Val Asp Phe Leu Lys Ala Gln Leu Gln Asn Ser Val Tyr Gly Val	
105 110 115	
acc acg ggt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc	438
Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val	
120 125 130	
agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg	486
Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro	
135 140 145 150	
acg tcc gyc tcg tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt	534
Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu	
155 160 165	
ccg ctc gag gtc gtc cgc ggc gcc atg gtc atc cgc gtc aac tcg ctc	582
Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu	
170 175 180	
acg cgt ggc cac tcg gcc gtc cgc ctc gtc gtc ctt gag gcg ctc acc	630
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr	
185 190 195	
aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc ggc tcc	678
Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser	
200 205 210	
atc tcg gcg tcg ggc gac ctc agc ccg ctc tcg tac atc gcc ggc gcc	726
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala	
215 220 225 230	

atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc	774
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr	
235 240 245	
gag aag atc atg ttt gcg cgc gag gcc atc tcg ctc ttt ggt ctc gag	822
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu	
250 255 260	
gca gtc gtc ctc ggc ccg aag gag ggt ctc ggt ctg gtc aac gga acg	870
Ala Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr	
265 270 275	
gcc gtc tcc gcc tcg atg gcg acc ctc agt ctg cac gac tcg cac atg	918
Ala Val Ser Ala Ser Met Ala Thr Leu Ser Leu His Asp Ser His Met	
280 285 290	
ctc tcg ctc ctc tcg cag gcc ttg acg gct ctc acg gtg gag gcc atg	966
Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met	
295 300 305 310	
gtc ggc cag cag ggc tcg ttc gcg ccg ttc atc cac gac gtc tgc cgc	1014
Val Gly Gln Gln Gly Ser Phe Ala Pro Phe Ile His Asp Val Cys Arg	
315 320 325	
ccg cac ccc ggc cag gtc gag gtc gcg cgc aac atc cgc acg ctc ctt	1062
Pro His Pro Gly Gln Val Glu Val Ala Arg Asn Ile Arg Thr Leu Leu	
330 335 340	
tcc ggc tcg tcg ttt gcc gtt gag cac gag gag gag gtc aag gtc aag	1110
Ser Gly Ser Ser Phe Ala Val Glu His Glu Glu Glu Val Lys Val Lys	
345 350 355	
gac gac gag ggc att ctt cgc cag gac cgc tac ccg ctc cgc acg tcg	1158
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser	
360 365 370	
cct cag ttc ctc ggc ccg ctc gtg gag gac atg atg cac gcc tac tcg	1206
Pro Gln Phe Leu Gly Pro Leu Val Glu Asp Met Met His Ala Tyr Ser	
375 380 385 390	

act ctc tcg ctc gag aac aac acg acg acc gac aac ccg ctc ctc gac	1254
Thr Leu Ser Leu Glu Asn Asn Thr Thr Thr Asp Asn Pro Leu Leu Asp	
395 400 405	
gtc gag aac aag cag acc gcg cac ggc ggc aac ttc cag gcg tcg gct	1302
Val Glu Asn Lys Gln Thr Ala His Gly Gly Asn Phe Gln Ala Ser Ala	
410 415 420	
gtc tcg att tcg atg gag aag acc agg ctc gca ctc gcc ctc atc ggc	1350
Val Ser Ile Ser Met Glu Lys Thr Arg Leu Ala Leu Ala Leu Ile Gly	
425 430 435	
aag ctc aac ttc acg cag tgc acc gag ttg ctc aac gct gcc atg aac	1398
Lys Leu Asn Phe Thr Gln Cys Thr Glu Leu Leu Asn Ala Ala Met Asn	
440 445 450	
cgc ggc ctg cct tcg tgc ctc gct gcc gag gac ccg tcg ctc aac tat	1446
Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Asn Tyr	
455 460 465 470	
cac ggc aag ggc ttg gac att cac atc gct gct tac gct tcg gag ctc	1494
His Gly Lys Gly Leu Asp Ile His Ile Ala Ala Tyr Ala Ser Glu Leu	
475 480 485	
ggc cac ctt gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg	1542
Gly His Leu Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met	
490 495 500	
ggc aac cag gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act	1590
Gly Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr	
505 510 515	
gcc gag gcc aac gac gtc ctt tct ctc ctt ctc gcc tcg cac ctg tac	1638
Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Ser His Leu Tyr	
520 525 530	
tgc acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag	1686
Cys Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys	
535 540 545 550	
aag cag ttc gac ccg ctt ctc ccg act ctc ctc cag cag cac ctc ggc	1734
Lys Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly	
555 560 565	

act ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc	1782
Thr Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu	
570 575 580	
aac aag cgt ctc gag cag acg acg acg tac gac ctc gag ccg cgc tgg	1830
Asn Lys Arg Leu Glu Gln Thr Thr Thr Tyr Asp Leu Glu Pro Arg Trp	
585 590 595	
cac gac gcc ttc tcg tac gcg acc ggc acc gtc gtc gag ctc ctc tcg	1878
His Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser	
600 605 610	
tcc tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag	1926
Ser Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys	
615 620 625 630	
gtt gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac	1974
Val Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn	
635 640 645	
cgc ttc tgg cag acg ccg tct tcg cag gcg ccg gcg cac gca tac ctc	2022
Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu	
650 655 660	
tcg ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc ggc	2070
Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly	
665 670 675	
gtg cag gcg cgc cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg	2118
Val Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr	
680 685 690	
atc ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc	2166
Ile Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg	
695 700 705 710	
atc aac cac gtc ctc gtc aag atg ctc gcg taaggcccg gcaagcctcg	2216
Ile Asn His Val Leu Val Lys Met Leu Ala	
715 720	
cctagacgcc cgcctcacc ccaagaccagc ttttcgacgt cgtgtcgtgc caagaacgga	2276

ctttcctcca tacacatgtc gccttactct ctgcgcgtca tcacgtctct cagttctttc 2336

gtatccccgag tctctcggtc gtcagtagac gtgtatagag cctggaatgg attgcaagtc 2396

ttcagattca aaaaaaaaaa aaa 2419

<210> 13

<211> 720

<212> PRT

<213> *Rhodotorula graminis*

<220>

<221> unsure

<222> (153)

<223> Other information: Xaa = Val or Ala

<400> 13

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	20							25					30		

Ser	Ala	Leu	Arg	Arg	Thr	Pro	Gly	Leu	Asp	Gly	His	Ala	Ala	His	Gln
	35						40					45			

Ser	Gln	Leu	Glu	Ile	Val	Gln	Glu	Leu	Leu	Ser	Asp	Pro	Thr	Asp	Asp
	50					55					60				

Val	Val	Glu	Leu	Ser	Gly	Tyr	Ser	Leu	Thr	Val	Arg	Asp	Val	Val	Gly
65					70					75					80

Ala	Ala	Arg	Lys	Gly	Arg	Arg	Val	Arg	Val	Gln	Asn	Asp	Asp	Glu	Ile
				85					90					95	

Arg	Ala	Arg	Val	Asp	Lys	Ser	Val	Asp	Phe	Leu	Lys	Ala	Gln	Leu	Gln
			100					105					110		

Asn	Ser	Val	Tyr	Gly	Val	Thr	Thr	Gly	Phe	Gly	Gly	Ser	Ala	Asp	Thr
		115					120						125		

Arg Thr Glu Asp Ala Val Ser Leu Gln Lys Ala Leu Ile Glu His Gln
 130 135 140

Leu Cys Gly Val Thr Pro Thr Ser Xaa Ser Ser Phe Ser Val Gly Arg
 145 150 155 160

Gly Leu Glu Asn Thr Leu Pro Leu Glu Val Val Arg Gly Ala Met Val
 165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Leu Val
 180 185 190

Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Arg Ile Thr Pro Ile
 195 200 205

Val Pro Leu Arg Gly Ser Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu
 210 215 220

Ser Tyr Ile Ala Gly Ala Ile Thr Gly His Pro Asp Val Lys Val His
 225 230 235 240

Val Leu His Glu Gly Thr Glu Lys Ile Met Phe Ala Arg Glu Ala Ile
 245 250 255

Ser Leu Phe Gly Leu Glu Ala Val Val Leu Gly Pro Lys Glu Gly Leu
 260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
 275 280 285

Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
 290 295 300

Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
 305 310 315 320

Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
 325 330 335

Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
 340 345 350

Glu	Glu	Val	Lys	Val	Lys	Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	Arg	355	360	365	
Tyr	Pro	Leu	Arg	Thr	Ser	Pro	Gln	Phe	Leu	Gly	Pro	Leu	Val	Glu	Asp	370	375	380	
Met	Met	His	Ala	Tyr	Ser	Thr	Leu	Ser	Leu	Glu	Asn	Asn	Thr	Thr	Thr	385	390	395	400
Asp	Asn	Pro	Leu	Leu	Asp	Val	Glu	Asn	Lys	Gln	Thr	Ala	His	Gly	Gly	405	410	415	
Asn	Phe	Gln	Ala	Ser	Ala	Val	Ser	Ile	Ser	Met	Glu	Lys	Thr	Arg	Leu	420	425	430	
Ala	Leu	Ala	Leu	Ile	Gly	Lys	Leu	Asn	Phe	Thr	Gln	Cys	Thr	Glu	Leu	435	440	445	
Leu	Asn	Ala	Ala	Met	Asn	Arg	Gly	Leu	Pro	Ser	Cys	Leu	Ala	Ala	Glu	450	455	460	
Asp	Pro	Ser	Leu	Asn	Tyr	His	Gly	Lys	Gly	Leu	Asp	Ile	His	Ile	Ala	465	470	475	480
Ala	Tyr	Ala	Ser	Glu	Leu	Gly	His	Leu	Ala	Asn	Pro	Val	Thr	Thr	Phe	485	490	495	
Val	Gln	Pro	Ala	Glu	Met	Gly	Asn	Gln	Ala	Val	Asn	Ser	Leu	Ala	Leu	500	505	510	
Ile	Ser	Ala	Arg	Arg	Thr	Ala	Glu	Ala	Asn	Asp	Val	Leu	Ser	Leu	Leu	515	520	525	
Leu	Ala	Ser	His	Leu	Tyr	Cys	Thr	Leu	Gln	Ala	Val	Asp	Leu	Arg	Ala	530	535	540	
Met	Glu	Leu	Asp	Phe	Lys	Lys	Gln	Phe	Asp	Pro	Leu	Leu	Pro	Thr	Leu	545	550	555	560
Leu	Gln	Gln	His	Leu	Gly	Thr	Gly	Leu	Asp	Val	Asn	Ala	Leu	Ala	Leu	565	570	575	

Glu Val Lys Lys Ala Leu Asn Lys Arg Leu Glu Gln Thr Thr Thr Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Tyr Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Pro Ser Ala Asn Val Thr Leu Thr
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Glu Val Arg Asn Arg Phe Trp Gln Thr Pro Ser Ser Gln Ala
645 650 655

Pro Ala His Ala Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Gln Ala Arg Arg Gly Asp Val Phe Val
675 680 685

Gly Val Gln Gln Glu Thr Ile Gly Ser Asn Val Ser Arg Ile Tyr Glu
690 695 700

Ala Ile Lys Asp Gly Arg Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720

<210> 14

<211> 2311

<212> DNA

<213> Amanita muscaria

<220>

<221> CDS

<222> (18)..(2237)

<400> 14

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Phe Phe Asp Leu Pro Lys Ala Val His Gly Met Asn Gly Thr Thr Pro	
15 20 25	
gtc aat ggt ttt aaa gcg aca gcg ctt tcc aag gcc tcc cga aca atg	146
Val Asn Gly Phe Lys Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met	
30 35 40	
acc aag act agc gca ctc tcg caa ttc tta gaa gcg tac cgt gaa ctc	194
Thr Lys Thr Ser Ala Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu	
45 50 55	
gag ggc tac aag aat ggt aga gcc atc aag gtt gac ggt caa acg tta	242
Glu Gly Tyr Lys Asn Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu	
60 65 70 75	
tct att gca gcc gtc gct gca gct gct cgc tac aat gcg gcc gtt gag	290
Ser Ile Ala Ala Val Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu	
80 85 90	
ttg gac gaa tcc cca ctt gtt aag gag cgc gtg agg aaa agt cag ctt	338
Leu Asp Glu Ser Pro Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu	
95 100 105	
gct atc gca aac aaa gta tcg acc ggt gcc agc gta tac gga ctg tca	386
Ala Ile Ala Asn Lys Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser	
110 115 120	
act ggt ttc ggt ggc agt gct gat aca cgg acg gac aaa ccg atg ttg	434
Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu	
125 130 135	
ttg ggg ttt gcc ctt ttg caa cac caa cat gta ggg ata ctg ccc acc	482
Leu Gly Phe Ala Leu Leu Gln His Gln His Val Gly Ile Leu Pro Thr	
140 145 150 155	
tcg act gag cct ttg gac gtc cta cct ctc caa gat gca aat aac aca	530
Ser Thr Glu Pro Leu Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr	
160 165 170	

agc atg cca gag gcg tgg att cgc ggg gcc att ttg atc cgt atg aat	578
Ser Met Pro Glu Ala Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn	
175 180 185	
tcg cta att cgt ggc cac tct gga atc aga tgg gag ttg atc gaa aag	626
Ser Leu Ile Arg Gly His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys	
190 195 200	
atg aga gaa cta ctc gcg gcc aat gtg ata cct gtc gtt ccc ctg aga	674
Met Arg Glu Leu Leu Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg	
205 210 215	
ggc agc atc tcc tca tcc gga gat ctg tct ccc cta tcc tat atc gca	722
Gly Ser Ile Ser Ser Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala	
220 225 230 235	
ggc acg att att ggc aac cca tca atc aag gta tat cac ggt cca tca	770
Gly Thr Ile Ile Gly Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser	
240 245 250	
aag tcc gga att cgc caa att gga tcc tcg aag gat gtc ttg gct ctg	818
Lys Ser Gly Ile Arg Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu	
255 260 265	
cat aat atc gaa cct ttc cca ctg gaa tcg aaa gaa cct ctt ggt att	866
His Asn Ile Glu Pro Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile	
270 275 280	
ttg aat ggg acc gca ttc tcg gca tct gtg gca gct tta gcc cta aac	914
Leu Asn Gly Thr Ala Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn	
285 290 295	
gaa gct atc cat ctt gtc ttg ttg gct caa gtg tgc acg gct atg ggg	962
Glu Ala Ile His Leu Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly	
300 305 310 315	
acc gag gca ttg ata ggc act cgc gct tct cat gca ccg ttc att cat	1010
Thr Glu Ala Leu Ile Gly Thr Arg Ala Ser His Ala Pro Phe Ile His	
320 325 330	
gcc acc gca cga cca cat ccc ggt caa gta gaa tgt gct gag aac att	1058
Ala Thr Ala Arg Pro His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile	
335 340 345	

tgg aat ttg ctc gat ggg agt aaa ttg gct cag tta gaa gag cac gaa	1106
Trp Asn Leu Leu Asp Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu	
350 355 360	
gtt cgc cta gaa gac gat aaa tac acc ctt cgg cag gac cgt tat cca	1154
Val Arg Leu Glu Asp Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro	
365 370 375	
ctc cga act tcg cct caa ttc ctt ggg cct cag att gaa gac ata atc	1202
Leu Arg Thr Ser Pro Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile	
380 385 390 395	
tcc gct ttc cag act gta acg cag gag tgt aat tac tta cca gct act	1250
Ser Ala Phe Gln Thr Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr	
400 405 410	
gac aat cca ctg att gat ggg gag act ggc gaa tct cac cac ggt ggc	1298
Asp Asn Pro Leu Ile Asp Gly Glu Thr Gly Glu Ser His His Gly Gly	
415 420 425	
aat ttc caa gcg atg gct gta act aat gca atg gag aag acg cga ctt	1346
Asn Phe Gln Ala Met Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu	
430 435 440	
gct tta cat cac gtt ggc aaa tta cta ttt tcc cag agc act gaa tta	1394
Ala Leu His His Val Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu	
445 450 455	
gtc aat cct gcg atg aac cgc ggt ctg ccg cct tca gta gct gcc aca	1442
Val Asn Pro Ala Met Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr	
460 465 470 475	
gat cca tct ctc aac tac cac gcc aaa gga cta gac ata gca act gcg	1490
Asp Pro Ser Leu Asn Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala	
480 485 490	
gcc tac gta gcc gaa gcg act cct ggc ccc act cac att cag tcg gca	1538
Ala Tyr Val Ala Glu Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala	
495 500 505	

gaa atg cac aac caa gct gtt aac tcc ctg gcg ttg att tct gct cgg	1586
Glu Met His Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg	
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gct acc atc aca tcg ttg gaa gtg cta aca tct ctg atc gcg tct tac	1634
Ala Thr Ile Thr Ser Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr	
525 530 535	
ttg tat att cta tgc caa gct ctc gac ctc cgt gcc ctt cag cgc gag	1682
Leu Tyr Ile Leu Cys Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu	
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ttc ttg ccc ggt cta gac atc atc att cgt gag gag tta aga tcg tca	1730
Phe Leu Pro Gly Leu Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser	
560 565 570	
ttt gga tct ttc ctg tca tca gaa cag atg gag aaa ttg caa caa aat	1778
Phe Gly Ser Phe Leu Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn	
575 580 585	
cta act agt gca ttt gaa gat cat ctt gac aag acc acg aca atg gat	1826
Leu Thr Ser Ala Phe Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp	
590 595 600	
aat act gat cga atg act acg atg gct gct aca tca tca tca gtt cta	1874
Asn Thr Asp Arg Met Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu	
605 610 615	
ctt caa ttc ttt act gat tct ggc gcg tct gtt cct ccc tcg tct tgc	1922
Leu Gln Phe Phe Thr Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys	
620 625 630 635	
gat ctt ctc tcc agt gtc tcg tcc ttc caa tct tct gtg gcg aca cgg	1970
Asp Leu Leu Ser Ser Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg	
640 645 650	
tct tca gtt ctc atg gat gac cta cgg aaa gaa tat att ttt gga gac	2018
Ser Ser Val Leu Met Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp	
655 660 665	
cgt ggc ccc acg ccc gca agc caa tac atc gga aag aca cgg cca gta	2066
Arg Gly Pro Thr Pro Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val	
670 675 680	

tac caa ttc att aga aca act ata ggc gtt cgt aag cat ggt tct gag 2114
 Tyr Gln Phe Ile Arg Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu
 685 690 695

aac tac aac aag ttt tat aat ggg ctg ggt gtc gaa gac gtt acc atc 2162
 Asn Tyr Asn Lys Phe Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile
 700 705 710 715

ggc caa aat ata tca cgc ata tac gag tca atc cgg gac ggc aaa atg 2210
 Gly Gln Asn Ile Ser Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met
 720 725 730

caa tcc att att gtc tcg ttg ttt gat taggtcttga aagcttgtat 2257
 Gln Ser Ile Ile Val Ser Leu Phe Asp
 735 740

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<210> 15

<211> 740

<212> PRT

<213> Amanita muscaria

<400> 15

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Lys Ala Val His Gly Met Asn Gly Thr Thr Pro Val Asn Gly Phe Lys
 20 25 30

Ala Thr Ala Leu Ser Lys Ala Ser Arg Thr Met Thr Lys Thr Ser Ala
 35 40 45

Leu Ser Gln Phe Leu Glu Ala Tyr Arg Glu Leu Glu Gly Tyr Lys Asn
 50 55 60

Gly Arg Ala Ile Lys Val Asp Gly Gln Thr Leu Ser Ile Ala Ala Val
 65 70 75 80

Ala Ala Ala Ala Arg Tyr Asn Ala Ala Val Glu Leu Asp Glu Ser Pro
 85 90 95

Leu Val Lys Glu Arg Val Arg Lys Ser Gln Leu Ala Ile Ala Asn Lys
 100 105 110

Val Ser Thr Gly Ala Ser Val Tyr Gly Leu Ser Thr Gly Phe Gly Gly
 115 120 125

Ser Ala Asp Thr Arg Thr Asp Lys Pro Met Leu Leu Gly Phe Ala Leu
 130 135 140

Leu Gln His Gln His Val Gly Ile Leu Pro Thr Ser Thr Glu Pro Leu
 145 150 155 160

Asp Val Leu Pro Leu Gln Asp Ala Asn Asn Thr Ser Met Pro Glu Ala
 165 170 175

Trp Ile Arg Gly Ala Ile Leu Ile Arg Met Asn Ser Leu Ile Arg Gly
 180 185 190

His Ser Gly Ile Arg Trp Glu Leu Ile Glu Lys Met Arg Glu Leu Leu
 195 200 205

Ala Ala Asn Val Ile Pro Val Val Pro Leu Arg Gly Ser Ile Ser Ser
 210 215 220

Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Thr Ile Ile Gly
 225 230 235 240

Asn Pro Ser Ile Lys Val Tyr His Gly Pro Ser Lys Ser Gly Ile Arg
 245 250 255

Gln Ile Gly Ser Ser Lys Asp Val Leu Ala Leu His Asn Ile Glu Pro
 260 265 270

Phe Pro Leu Glu Ser Lys Glu Pro Leu Gly Ile Leu Asn Gly Thr Ala
 275 280 285

Phe Ser Ala Ser Val Ala Ala Leu Ala Leu Asn Glu Ala Ile His Leu
 290 295 300

Val Leu Leu Ala Gln Val Cys Thr Ala Met Gly Thr Glu Ala Leu Ile
 305 310 315 320

Gly Thr Arg Ala Ser His Ala Pro Phe Ile His Ala Thr Ala Arg Pro			
325	330	335	
His Pro Gly Gln Val Glu Cys Ala Glu Asn Ile Trp Asn Leu Leu Asp			
340	345	350	
Gly Ser Lys Leu Ala Gln Leu Glu Glu His Glu Val Arg Leu Glu Asp			
355	360	365	
Asp Lys Tyr Thr Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser Pro			
370	375	380	
Gln Phe Leu Gly Pro Gln Ile Glu Asp Ile Ile Ser Ala Phe Gln Thr			
385	390	395	400
Val Thr Gln Glu Cys Asn Tyr Leu Pro Ala Thr Asp Asn Pro Leu Ile			
405	410	415	
Asp Gly Glu Thr Gly Glu Ser His His Gly Gly Asn Phe Gln Ala Met			
420	425	430	
Ala Val Thr Asn Ala Met Glu Lys Thr Arg Leu Ala Leu His His Val			
435	440	445	
Gly Lys Leu Leu Phe Ser Gln Ser Thr Glu Leu Val Asn Pro Ala Met			
450	455	460	
Asn Arg Gly Leu Pro Pro Ser Val Ala Ala Thr Asp Pro Ser Leu Asn			
465	470	475	480
Tyr His Ala Lys Gly Leu Asp Ile Ala Thr Ala Ala Tyr Val Ala Glu			
485	490	495	
Ala Thr Pro Gly Pro Thr His Ile Gln Ser Ala Glu Met His Asn Gln			
500	505	510	
Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Ala Thr Ile Thr Ser			
515	520	525	
Leu Glu Val Leu Thr Ser Leu Ile Ala Ser Tyr Leu Tyr Ile Leu Cys			
530	535	540	

Gln Ala Leu Asp Leu Arg Ala Leu Gln Arg Glu Phe Leu Pro Gly Leu
 545 550 555 560

Asp Ile Ile Ile Arg Glu Glu Leu Arg Ser Ser Phe Gly Ser Phe Leu
 565 570 575

Ser Ser Glu Gln Met Glu Lys Leu Gln Gln Asn Leu Thr Ser Ala Phe
 580 585 590

Glu Asp His Leu Asp Lys Thr Thr Thr Met Asp Asn Thr Asp Arg Met
 595 600 605

Thr Thr Met Ala Ala Thr Ser Ser Ser Val Leu Leu Gln Phe Phe Thr
 610 615 620

Asp Ser Gly Ala Ser Val Pro Pro Ser Ser Cys Asp Leu Leu Ser Ser
 625 630 635 640

Val Ser Ser Phe Gln Ser Ser Val Ala Thr Arg Ser Ser Val Leu Met
 645 650 655

Asp Asp Leu Arg Lys Glu Tyr Ile Phe Gly Asp Arg Gly Pro Thr Pro
 660 665 670

Ala Ser Gln Tyr Ile Gly Lys Thr Arg Pro Val Tyr Gln Phe Ile Arg
 675 680 685

Thr Thr Ile Gly Val Arg Lys His Gly Ser Glu Asn Tyr Asn Lys Phe
 690 695 700

Tyr Asn Gly Leu Gly Val Glu Asp Val Thr Ile Gly Gln Asn Ile Ser
 705 710 715 720

Arg Ile Tyr Glu Ser Ile Arg Asp Gly Lys Met Gln Ser Ile Ile Val
 725 730 735

Ser Leu Phe Asp
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<210> 16
 <211> 2787
 <212> DNA

<213> Rhodotorula mucilaginosa

<220>

<221> CDS

<222> (646)..(2784)

<400> 16

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tcggcttggt cctctcctct atagacatgg gtactgatca cttegtttgt tgttctcggt 180
ttctcttgca agtacgaccc atcctttttt ctgcgcatcg acttcaatat cggcgcgctt 240
gcactacgtc tcttcgccag tgcacagtat gacgggaggg gacacgactg gcggcgaaaag 300
cggagtcgtc gttgccggtc ccgagagacg ggaacacttt ctccgcctt ccagaggccg 360
tactccggtg atttgacatc gcactatgct tgggtggggcg cccgaactcg gagcttgca 420
tgtgcctgaa gcagagctcg gcaggcgaca tggcgactcc gccacattcg ggtcaaagcc 480
gaagtggggc ctcggaagtt ccgaacgtcg tcttgccgcc gccgcgttgc gtccgccgtc 540
gactttgtcc tcgtgtgtc acgcctcctt cttctctctt tctgctttcc tcacttcact 600
ctgcaagtcc cgctcgcat ccaccaacc cgagcagctc tcaag atg gcc ccc tcc 657
Met Ala Pro Ser

1

gtc gac tcg atc gcg act tcg gtt gcc aac tcc ctc tcg aac ggg ttg 705
Val Asp Ser Ile Ala Thr Ser Val Ala Asn Ser Leu Ser Asn Gly Leu
5 10 15 20

cac gcc gcc gcc gcc gcc aac ggt ggc gac gtc cac aag aag acg gcc 753
His Ala Ala Ala Ala Ala Asn Gly Gly Asp Val His Lys Lys Thr Ala
25 30 35

ggt gct ggc tcc ctc ctc ccg acc acc gag acg acc cag ctc gac atc 801
Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr Gln Leu Asp Ile
40 45 50

gtt gag cgc atc ttg gcc gac gcc ggc gcg acg gac cag atc aaa ctc	849
Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp Gln Ile Lys Leu	
55 60 65	
gat ggg tac acc ctc acg ctc ggc gac gtc gtc ggc gct gct cgc cgt	897
Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly Ala Ala Arg Arg	
70 75 80	
ggc cgc tcc gtc aag gtc gca gac agc ccg cac atc cgc gag aag atc	945
Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile Arg Glu Lys Ile	
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gat gcc agt gtc gag ttc ctc cgt act cag ctc gac aac agt gtc tac	993
Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp Asn Ser Val Tyr	
105 110 115	
ggc gtc acg act ggt ttc ggc ggc tcg gcc gac acc cgg act gag gat	1041
Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp	
120 125 130	
gcg atc tcg ctc caa aag gcc ctg ctc gag cac cag ctc tgc ggt gtc	1089
Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val	
135 140 145	
ctc ccc acc tcg atg gat ggc ttt gcg ctc ggt cgc ggc ctc gag aac	1137
Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg Gly Leu Glu Asn	
150 155 160	
tcg ctt ccg ctc gaa gtc gtc cga ggc gcg atg acc atc cgt gtc aac	1185
Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn	
165 170 175 180	
tcg ctc act cgc ggt cac tcg gcg gtc cgc atc gtc gtc ctc gaa gcc	1233
Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val Val Leu Glu Ala	
185 190 195	
ctc acc aac ttc ctc aac cac ggc atc acc ccg atc gtc ccg ctt cga	1281
Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg	
200 205 210	

ggc acc atc tcg gcg tcg ggc gac ctt tcc ccc ctc tct tac atc gcc	1329
Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala	
215 220 225	
gcc tcg atc acc ggc cac ccg gac tcg aag gtc cac gtc gac ggc aag	1377
Ala Ser Ile Thr Gly His Pro Asp Ser Lys Val His Val Asp Gly Lys	
230 235 240	
atc atg tcc gcc cag gag gcg atc gcg ctc aag ggt ctt cag ccc gtc	1425
Ile Met Ser Ala Gln Glu Ala Ile Ala Leu Lys Gly Leu Gln Pro Val	
245 250 255 260	
gtc ctc ggt ccg aag gag ggt ctc ggt ctc gtc aac ggc acg gcc gtc	1473
Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr Ala Val	
265 270 275	
tcc gcc tcg atg gcg acg ctg gcc ctc acc gac gca cac gtc ctc tcg	1521
Ser Ala Ser Met Ala Thr Leu Ala Leu Thr Asp Ala His Val Leu Ser	
280 285 290	
ctc ctc gca cag gcg ctc act gct ctt act gtc gag gcc atg gtc gga	1569
Leu Leu Ala Gln Ala Leu Thr Ala Leu Thr Val Glu Ala Met Val Gly	
295 300 305	
cac gcc ggc tcg ttc cac cca ttc ctc cac gac gtc acg cgc cct cac	1617
His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg Pro His	
310 315 320	
ccg acc cag atc gag gtg gcg cgc aac atc cgg act ctt ctc gag ggc	1665
Pro Thr Gln Ile Glu Val Ala Arg Asn Ile Arg Thr Leu Leu Glu Gly	
325 330 335 340	
agc aag tac gcc gtc cac cac gag act gaa gtc aag gtc aag gac gac	1713
Ser Lys Tyr Ala Val His His Glu Thr Glu Val Lys Val Lys Asp Asp	
345 350 355	
gag ggc atc ctc agg cag gac cgg tac ccg ctc cgc tgc tcg ccg cag	1761
Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Cys Ser Pro Gln	
360 365 370	
tgg ctc ggt ccc ctt gtc agc gac atg att cac gct cac gct gtc ctc	1809
Trp Leu Gly Pro Leu Val Ser Asp Met Ile His Ala His Ala Val Leu	
375 380 385	

tcg ctc gag gct ggt cag tcg acc acc gac aac ccg ctg atc gac ctc	1857
Ser Leu Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile Asp Leu	
390 395 400	
 gag aac aag atg acc cac cat ggc gga gcc ttc atg gcg agc agc gtc	1905
Glu Asn Lys Met Thr His His Gly Gly Ala Phe Met Ala Ser Ser Val	
405 410 415 420	
 gga aac acg atg gag aag act cgc ctc gcc gtc gcg ctg atg ggc aag	1953
Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala Leu Met Gly Lys	
425 430 435	
 gtc agc ttt act cag ctc acc gag atg ctc aac gcc ggc atg aac cgg	2001
Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met Asn Arg	
440 445 450	
 gcc ctt ccg tcc tgc ctc gct gcc gag gac cct tcc ctc tct tat cac	2049
Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser Tyr His	
455 460 465	
 tgc aag ggt ctc gac att gct gcg gcc gcc tac act tcc gag ctc ggt	2097
Cys Lys Gly Leu Asp Ile Ala Ala Ala Tyr Thr Ser Glu Leu Gly	
470 475 480	
 cac ctt gcc aac ccg gtt tcg acc cac gtc cag ccg gcc gag atg ggc	2145
His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro Ala Glu Met Gly	
485 490 495 500	
 aac cag gcc atc aac tcg ctc gcc ctc atc tcg gcc cgc cgc acc gcc	2193
Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala	
505 510 515	
 gag gcg aac gac gtt ctc tcc ctc ctc ctc gcc acc cac ctc tac tgc	2241
Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu Tyr Cys	
520 525 530	
 gtc ctc cag gcc gtc gac ctc cgc gcg atg gag ttt gag cac acc aag	2289
Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe Glu His Thr Lys	
535 540 545	

gcg ttc gag ccg atg gtc act gag ctg ttg aag cag cac ttt ggc gcg	2337
Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln His Phe Gly Ala	
550 555 560	
ctc gcg acg gcc gaa gtc gag gac aag gtc cgc aag tcg atc tac aag	2385
Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys Ser Ile Tyr Lys	
565 570 575 580	
cgg ttg cag cag aac aac tcg tac gac ctc gag cag cgg tgg cac gac	2433
Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln Arg Trp His Asp	
585 590 595	
acg ttc tcg gtc gcg acc ggt gcc gtc gtc gag gcg ctc gcc ggc cag	2481
Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala Leu Ala Gly Gln	
600 605 610	
gag gtc tcg ctc gcg agc ctc aac gcc tgg aag gtc gcc tgc gcc gag	2529
Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val Ala Cys Ala Glu	
615 620 625	
aag gct atc gcg ctc acg cgc tcc gtc cgc gac tcg ttc tgg gcg gct	2577
Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser Phe Trp Ala Ala	
630 635 640	
ccg tcg tcg tcg tcg ccc gcg ctc aag tac ctc tcc ccg cgg acg cgc	2625
Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser Pro Arg Thr Arg	
645 650 655 660	
gtc ctg tat tcg ttc gtc cgg gag gag gtc ggc gtc aag gcc cgc cgc	2673
Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val Lys Ala Arg Arg	
665 670 675	
ggc gat gtc tac ctc ggc aag cag gag gtc acg atc ggc acc aac gtc	2721
Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val	
680 685 690	
agc cgc atc tac gag gcg atc aag agc ggt tgc atc gcc ccc gtc ctc	2769
Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile Ala Pro Val Leu	
695 700 705	
gtc aag atg atg gca tag	2787
Val Lys Met Met Ala	
710	

<210> 17

<211> 713

<212> PRT

<213> Rhodotorula mucilaginosa

<400> 17

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20 25 30

Lys Lys Thr Ala Gly Ala Gly Ser Leu Leu Pro Thr Thr Glu Thr Thr
35 40 45

Gln Leu Asp Ile Val Glu Arg Ile Leu Ala Asp Ala Gly Ala Thr Asp
50 55 60

Gln Ile Lys Leu Asp Gly Tyr Thr Leu Thr Leu Gly Asp Val Val Gly
65 70 75 80

Ala Ala Arg Arg Gly Arg Ser Val Lys Val Ala Asp Ser Pro His Ile
85 90 95

Arg Glu Lys Ile Asp Ala Ser Val Glu Phe Leu Arg Thr Gln Leu Asp
100 105 110

Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr
115 120 125

Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln
130 135 140

Leu Cys Gly Val Leu Pro Thr Ser Met Asp Gly Phe Ala Leu Gly Arg
145 150 155 160

Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr
165 170 175

Ile Arg Val Asn Ser Leu Thr Arg Gly His Ser Ala Val Arg Ile Val
180 185 190

Val	Leu	Glu	Ala	Leu	Thr	Asn	Phe	Leu	Asn	His	Gly	Ile	Thr	Pro	Ile	195	200	205	
Val	Pro	Leu	Arg	Gly	Thr	Ile	Ser	Ala	Ser	Gly	Asp	Leu	Ser	Pro	Leu	210	215	220	
Ser	Tyr	Ile	Ala	Ala	Ser	Ile	Thr	Gly	His	Pro	Asp	Ser	Lys	Val	His	225	230	235	240
Val	Asp	Gly	Lys	Ile	Met	Ser	Ala	Gln	Glu	Ala	Ile	Ala	Leu	Lys	Gly	245	250	255	
Leu	Gln	Pro	Val	Val	Leu	Gly	Pro	Lys	Glu	Gly	Leu	Gly	Leu	Val	Asn	260	265	270	
Gly	Thr	Ala	Val	Ser	Ala	Ser	Met	Ala	Thr	Leu	Ala	Leu	Thr	Asp	Ala	275	280	285	
His	Val	Leu	Ser	Leu	Leu	Ala	Gln	Ala	Leu	Thr	Ala	Leu	Thr	Val	Glu	290	295	300	
Ala	Met	Val	Gly	His	Ala	Gly	Ser	Phe	His	Pro	Phe	Leu	His	Asp	Val	305	310	315	320
Thr	Arg	Pro	His	Pro	Thr	Gln	Ile	Glu	Val	Ala	Arg	Asn	Ile	Arg	Thr	325	330	335	
Leu	Leu	Glu	Gly	Ser	Lys	Tyr	Ala	Val	His	His	Glu	Thr	Glu	Val	Lys	340	345	350	
Val	Lys	Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	Arg	Tyr	Pro	Leu	Arg	355	360	365	
Cys	Ser	Pro	Gln	Trp	Leu	Gly	Pro	Leu	Val	Ser	Asp	Met	Ile	His	Ala	370	375	380	
His	Ala	Val	Leu	Ser	Leu	Glu	Ala	Gly	Gln	Ser	Thr	Thr	Asp	Asn	Pro	385	390	395	400
Leu	Ile	Asp	Leu	Glu	Asn	Lys	Met	Thr	His	His	Gly	Gly	Ala	Phe	Met	405	410	415	

Ala Ser Ser Val Gly Asn Thr Met Glu Lys Thr Arg Leu Ala Val Ala	420	425	430
Leu Met Gly Lys Val Ser Phe Thr Gln Leu Thr Glu Met Leu Asn Ala	435	440	445
Gly Met Asn Arg Ala Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser	450	455	460
Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr	465	470	475 480
Ser Glu Leu Gly His Leu Ala Asn Pro Val Ser Thr His Val Gln Pro	485	490	495
Ala Glu Met Gly Asn Gln Ala Ile Asn Ser Leu Ala Leu Ile Ser Ala	500	505	510
Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser Leu Leu Leu Ala Thr	515	520	525
His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu Arg Ala Met Glu Phe	530	535	540
Glu His Thr Lys Ala Phe Glu Pro Met Val Thr Glu Leu Leu Lys Gln	545	550	555 560
His Phe Gly Ala Leu Ala Thr Ala Glu Val Glu Asp Lys Val Arg Lys	565	570	575
Ser Ile Tyr Lys Arg Leu Gln Gln Asn Asn Ser Tyr Asp Leu Glu Gln	580	585	590
Arg Trp His Asp Thr Phe Ser Val Ala Thr Gly Ala Val Val Glu Ala	595	600	605
Leu Ala Gly Gln Glu Val Ser Leu Ala Ser Leu Asn Ala Trp Lys Val	610	615	620
Ala Cys Ala Glu Lys Ala Ile Ala Leu Thr Arg Ser Val Arg Asp Ser	625	630	635 640

Phe Trp Ala Ala Pro Ser Ser Ser Ser Pro Ala Leu Lys Tyr Leu Ser
645 650 655

Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Val Gly Val
660 665 670

Lys Ala Arg Arg Gly Asp Val Tyr Leu Gly Lys Gln Glu Val Thr Ile
675 680 685

Gly Thr Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Cys Ile
690 695 700

Ala Pro Val Leu Val Lys Met Met Ala
705 710

<210> 18

<211> 2439

<212> DNA

<213> Rhodotorula toruloides

<220>

<221> CDS

<222> (1)..(2148)

<400> 18

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gca tcc gca aag cag gct gtc aat ggc gcc tcg acc aac ctc gca gtc 96
Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
20 25 30

gca ggc tcg cac ctg ccc aca acc cag gtc acg cag gtc gac atc gtc 144
Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
35 40 45

gag aag atg ctc gcc gcg ccg acc gac tcg acg ctc gaa ctc gac ggc 192
Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
50 55 60

atc	agc	ggc	cac	ccg	gac	agc	aag	gtg	cac	gtc	gtc	cac	gag	ggc	aag	720
Ile	Ser	Gly	His	Pro	Asp	Ser	Lys	Val	His	Val	Val	His	Glu	Gly	Lys	
225					230					235					240	
gag	aag	atc	ctg	tac	gcc	cgc	gag	gcg	atg	gcg	ctc	ttc	aac	ctc	gag	768
Glu	Lys	Ile	Leu	Tyr	Ala	Arg	Glu	Ala	Met	Ala	Leu	Phe	Asn	Leu	Glu	
				245					250					255		
ccc	gtc	gtc	ctc	ggc	ccg	aag	gaa	ggc	ctc	ggc	ctc	gtc	aac	ggc	acc	816
Pro	Val	Val	Leu	Gly	Pro	Lys	Glu	Gly	Leu	Gly	Leu	Val	Asn	Gly	Thr	
			260					265					270			
gcc	gtc	tca	gca	tcg	atg	gcc	acc	ctc	gct	ctg	cac	gac	gca	cac	atg	864
Ala	Val	Ser	Ala	Ser	Met	Ala	Thr	Leu	Ala	Leu	His	Asp	Ala	His	Met	
		275					280					285				
ctc	tcg	ctc	ctc	tcg	cag	tcg	ctc	acg	gcc	atg	acg	gtc	gaa	gcg	atg	912
Leu	Ser	Leu	Leu	Ser	Gln	Ser	Leu	Thr	Ala	Met	Thr	Val	Glu	Ala	Met	
	290					295					300					
gtc	ggc	cac	gcc	ggc	tcg	ttc	cac	ccc	ttc	ctt	cac	gac	gtc	acg	cgc	960
Val	Gly	His	Ala	Gly	Ser	Phe	His	Pro	Phe	Leu	His	Asp	Val	Thr	Arg	
305					310					315					320	
cct	cac	ccg	acg	cag	atc	gaa	gtc	gcg	gga	aac	atc	cgc	aag	ctc	ctc	1008
Pro	His	Pro	Thr	Gln	Ile	Glu	Val	Ala	Gly	Asn	Ile	Arg	Lys	Leu	Leu	
				325					330					335		
gag	gga	agc	cgc	ttt	gct	gtc	cac	cat	gag	gag	gag	gtc	aag	gtc	aag	1056
Glu	Gly	Ser	Arg	Phe	Ala	Val	His	His	Glu	Glu	Glu	Val	Lys	Val	Lys	
			340					345					350			
gac	gac	gag	ggc	att	ctc	cgc	cag	gac	cgc	tac	ccc	ttg	cgc	acg	tct	1104
Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	Arg	Tyr	Pro	Leu	Arg	Thr	Ser	
		355					360					365				
cct	cag	tgg	ctc	ggc	ccg	ctc	gtc	agc	gac	ctc	att	cac	gcc	cac	gcc	1152
Pro	Gln	Trp	Leu	Gly	Pro	Leu	Val	Ser	Asp	Leu	Ile	His	Ala	His	Ala	
	370					375					380					
gtc	ctc	acc	atc	gag	gcc	ggc	cag	tcg	acg	acc	gac	aac	cct	ctc	atc	1200
Val	Leu	Thr	Ile	Glu	Ala	Gly	Gln	Ser	Thr	Thr	Asp	Asn	Pro	Leu	Ile	
385					390					395					400	

gac gtc gag aac aag act tcg cac cac ggc ggc aat ttc cag gct gcc	1248
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala	
405 410 415	
gct gtg gcc aac acc atg gag aag act cgc ctc ggg ctc gcc cag atc	1296
Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile	
420 425 430	
ggc aag ctc aac ttc acg cag ctc acc gag atg ctc aac gcc ggc atg	1344
Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met	
435 440 445	
aac cgc ggc ctc ccc tcc tgc ctc gcg gcc gaa gac ccc tcg ctc tcc	1392
Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser	
450 455 460	
tac cac tgc aag ggc ctc gac atc gcc gct gcg gcg tac acc tcg gag	1440
Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu	
465 470 475 480	
ttg gga cac ctc gcc aac cct gtg acg acg cat gtc cag ccg gct gag	1488
Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu	
485 490 495	
atg gcg aac cag gcg gtc aac tcg ctt gcg ctc atc tcg gct cgt cgc	1536
Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg	
500 505 510	
acg acc gag tcc aac gac gtc ctt tct ctc ctc ctc gcc acc cac ctc	1584
Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu	
515 520 525	
tac tgc gtt ctc caa gcc atc gac ttg cgc gcg atc gag ttc gag ttc	1632
Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe	
530 535 540	
aag aag cag ttc ggc cca gcc atc gtc tcg ctc atc gac cag cac ttt	1680
Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe	
545 550 555 560	

ggc tcc gcc atg acc ggc tcg aac ctg cgc gac gag ctc gtc gag aag	1728
Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys	
565 570 575	
gtg aac aag acg ctc gcc aag cgc ctc gag cag acc aac tcg tac gac	1776
Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp	
580 585 590	
ctc gtc ccg cgc tgg cac gac gcc ttc tcc ttc gcc gcc ggc acc gtc	1824
Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val	
595 600 605	
gtc gag gtc ctc tcg tcg acg tcg ctc tcg ctc gcc gcc gtc aac gcc	1872
Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala	
610 615 620	
tgg aag gtc gcc gcc gcc gag tcg gcc atc tcg ctc acc cgc caa gtc	1920
Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val	
625 630 635 640	
cgc gag acc ttc tgg tcc gcc gcg tcg acc tcg tcg ccc gcg ctc tcg	1968
Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser	
645 650 655	
tac ctc tcg ccg cgc act cag atc ctc tac gcc ttc gtc cgc gag gag	2016
Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu	
660 665 670	
ctt ggc gtc aag gcc cgc cgc gga gac gtc ttc ctc ggc aag caa gag	2064
Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu	
675 680 685	
gtg acg atc ggc tcg aac gtc tcc aag atc tac gag gcc atc aag tcg	2112
Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser	
690 695 700	
ggc agg atc aac aac gtc ctc ctc aag atg ctc gct tagacactct	2158
Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala	
705 710 715	
tcccactctc gcatecccttc cataccctat ccgcctgca ctcttaggac tcgcttcttg	2218
tcggactcgg atctcgcatc gcttctttcg ttcttggtg cctctctaga ccgtgtccgt	2278

attacctega gattgtgaat acaagcagta cccatccacg catccgataa atcagggaga 2338
 gaatctacgc ttgcgggagc ttcttgcgca taaactgtcg agtgcgggcg ttagtgcgaa 2398
 gtcaacgaag gcgagtggca gcggctcact accgcctega g 2439

<210> 19
 <211> 716
 <212> PRT
 <213> Rhodotorula toruloides

<400> 19
 Met Ala Pro Ser Leu Asp Ser Ile Scr His Ser Phe Ala Asn Gly Val
 1 5 10 15
 Ala Ser Ala Lys Gln Ala Val Asn Gly Ala Ser Thr Asn Leu Ala Val
 20 25 30
 Ala Gly Ser His Leu Pro Thr Thr Gln Val Thr Gln Val Asp Ile Val
 35 40 45
 Glu Lys Met Leu Ala Ala Pro Thr Asp Ser Thr Leu Glu Leu Asp Gly
 50 55 60
 Tyr Ser Leu Asn Leu Gly Asp Val Val Ser Ala Ala Arg Lys Gly Arg
 65 70 75 80
 Pro Val Arg Val Lys Asp Ser Asp Glu Ile Arg Ser Lys Ile Asp Lys
 85 90 95
 Ser Val Glu Phe Leu Arg Ser Gln Leu Ser Met Ser Val Tyr Gly Val
 100 105 110
 Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Ile
 115 120 125
 Ser Leu Gln Lys Ala Leu Leu Glu His Gln Leu Cys Gly Val Leu Pro
 130 135 140

Ser Ser Phe Asp Ser Phe Arg Leu Gly Arg Gly Leu Glu Asn Ser Leu			
145	150	155	160
Pro Leu Glu Val Val Arg Gly Ala Met Thr Ile Arg Val Asn Ser Leu			
	165	170	175
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr			
	180	185	190
Asn Phe Leu Asn His Gly Ile Thr Pro Ile Val Pro Leu Arg Gly Thr			
	195	200	205
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Ala Ala			
210	215	220	
Ile Ser Gly His Pro Asp Ser Lys Val His Val Val His Glu Gly Lys			
225	230	235	240
Glu Lys Ile Leu Tyr Ala Arg Glu Ala Met Ala Leu Phe Asn Leu Glu			
	245	250	255
Pro Val Val Leu Gly Pro Lys Glu Gly Leu Gly Leu Val Asn Gly Thr			
	260	265	270
Ala Val Ser Ala Ser Met Ala Thr Leu Ala Leu His Asp Ala His Met			
	275	280	285
Leu Ser Leu Leu Ser Gln Ser Leu Thr Ala Met Thr Val Glu Ala Met			
	290	295	300
Val Gly His Ala Gly Ser Phe His Pro Phe Leu His Asp Val Thr Arg			
305	310	315	320
Pro His Pro Thr Gln Ile Glu Val Ala Gly Asn Ile Arg Lys Leu Leu			
	325	330	335
Glu Gly Ser Arg Phe Ala Val His His Glu Glu Glu Val Lys Val Lys			
	340	345	350
Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg Tyr Pro Leu Arg Thr Ser			
	355	360	365

Pro Gln Trp Leu Gly Pro Leu Val Ser Asp Leu Ile His Ala His Ala			
370	375	380	
Val Leu Thr Ile Glu Ala Gly Gln Ser Thr Thr Asp Asn Pro Leu Ile			
385	390	395	400
Asp Val Glu Asn Lys Thr Ser His His Gly Gly Asn Phe Gln Ala Ala			
	405	410	415
Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu Gly Leu Ala Gln Ile			
	420	425	430
Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met Leu Asn Ala Gly Met			
	435	440	445
Asn Arg Gly Leu Pro Ser Cys Leu Ala Ala Glu Asp Pro Ser Leu Ser			
	450	455	460
Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala Ala Tyr Thr Ser Glu			
465	470	475	480
Leu Gly His Leu Ala Asn Pro Val Thr Thr His Val Gln Pro Ala Glu			
	485	490	495
Met Ala Asn Gln Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg			
	500	505	510
Thr Thr Glu Ser Asn Asp Val Leu Ser Leu Leu Leu Ala Thr His Leu			
	515	520	525
Tyr Cys Val Leu Gln Ala Ile Asp Leu Arg Ala Ile Glu Phe Glu Phe			
	530	535	540
Lys Lys Gln Phe Gly Pro Ala Ile Val Ser Leu Ile Asp Gln His Phe			
545	550	555	560
Gly Ser Ala Met Thr Gly Ser Asn Leu Arg Asp Glu Leu Val Glu Lys			
	565	570	575
Val Asn Lys Thr Leu Ala Lys Arg Leu Glu Gln Thr Asn Ser Tyr Asp			
	580	585	590

Leu Val Pro Arg Trp His Asp Ala Phe Ser Phe Ala Ala Gly Thr Val
595 600 605

Val Glu Val Leu Ser Ser Thr Ser Leu Ser Leu Ala Ala Val Asn Ala
610 615 620

Trp Lys Val Ala Ala Ala Glu Ser Ala Ile Ser Leu Thr Arg Gln Val
625 630 635 640

Arg Glu Thr Phe Trp Ser Ala Ala Ser Thr Ser Ser Pro Ala Leu Ser
645 650 655

Tyr Leu Ser Pro Arg Thr Gln Ile Leu Tyr Ala Phe Val Arg Glu Glu
660 665 670

Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu Gly Lys Gln Glu
675 680 685

Val Thr Ile Gly Ser Asn Val Ser Lys Ile Tyr Glu Ala Ile Lys Ser
690 695 700

Gly Arg Ile Asn Asn Val Leu Leu Lys Met Leu Ala
705 710 715

<210> 20

<211> 2475

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_difference

<222> (13) .. (2475)

<223> n = A or C or G or T; "n" indicates no consensus at that position

<223> Description of Artificial Sequence: Consensus
Sequence of SEQ ID NOS: 12, 16, and 18

<400> 20

atggcccccct cctgcgactc gatcgcgacc tcgntcgcca acggcctcnc naacggntng 60

cagcccgnc cgnennngnc gncnacgggc gccacgtcca cnetcngncg gccgncgncg 120
 gctcgctcct cccgaccacc cagnngacgc agctcgacat cgtngagnag atcctcgccg 180
 accccaccgn nacgnacggn ntcgaactcg acgggtacac cctcaccctc ggngacgtcg 240
 tcggcgccgc ncgcaagggc cgcncngtcc gcgtcncaga cagncgacga gatccgcgca 300
 aagatcgaca anagngtcga gttcctccgn nncagctcn acaacagngt ctacggngtc 360
 acgactgggt tcggcggtc ggccgacacc cggactgagg atgcnatctc gctccagaag 420
 gcnctcctcg agcaccagct ctggggtgtn ctccnacgt cgnctcgantc cttcngcctc 480
 ggncgcggcc tcgagaactc gttcctcgct gaggtcgctc gcggcgccat gaccatccgc 540
 gtcaactcgc tcacncgcgg ccactcggcn gtccgcctcg tcgtcctcga ggcgctcacc 600
 aacttctca accacggcat ccccccatc gtccccctcc gcggcaccat ctgggcgtcg 660
 ggcgacctct cccnctctc ntacatcgcc gccgccatca ccggtcaccc ggacnncaag 720
 gtncacgtnn tncacgaggg canngagaag atcatgtncg cccgcgaggg gatcgcgctc 780
 ttnggtctcg agcccgctgt cctcgggccg aaggagggtc tcgggtctgt caacggcacg 840
 gccgtctcgg cctcgatggc gaccctcgct ctgcacgacg cacacatgct ctcgctcctc 900
 tcgcaggcgc tcacggctct nacggtcgag gccatggctg gccacgccgg ctcggtccac 960
 ccnttctcc acgacgtcac gcgcctcac ccgaccaga tcgaggtcgc gcgcaacatc 1020
 cgcacgtcc tcgagggcag cnggtttgcc gtccaccacg aggaggaggt caaggtcaag 1080
 gacgacgagg gcattctcc ccaggaccgc taccgctcc gcacgtcgcc tcagtggctc 1140
 ggcccgtcg tcagcgacat gattcacgcc cagcngtcc tctcgctcga ggccggncag 1200
 tcgacgaccg acaaccgct catcgacgtc gagaacaaga ngaccacca cggcggaac 1260
 ttccaggcgn ccgctgtcg naacacgatg gagaagactc gcctcgcnet cgccctgatc 1320
 ggcaagctca acttcacgca gtcaccgag atgtcaacg ccggcatgaa ccgcggcctn 1380

centcctgcc tcgctgccga ggaccntcg ctctctatc actgcaaggg cctcgacatt 1440
gccgngcng cntacaette ggagctcggg caccttgcca acccggtnac gacccacgtc 1500
cagccggcng agatgggcaa ccaggccgtc aactcgctcg cnetcatctc ggcncgccgc 1560
acngccgagg ccaacgacgt cctttctctc ctctcgcca cccaccteta ctgctnctc 1620
caggccgtcg acctccgcgc gatggagttc gaggtaaga agcagttcga cccgntnntc 1680
nncncgctcn tcnagcagca ctttggcncn gccctcgacg gcnnnnnnnn nnnnnacgaa 1740
ctcngggaca aggtcaacaa gncgctcnac aagcgnctcg agcagaccaa ctcgtagcac 1800
ctcgagccgc gctggcacga cgccttctcg ttcgcgaccg gcaccgtcgt cgagnnnnnn 1860
nngtcctcgc cnnngccan naggtctcgc tcgncgccgt caacgcctgg aaggtcgcct 1920
ccgccgagaa ggccatctcg ctacgcgcn angtcgcga cnccttctgg ncggncgcgt 1980
cgtcgtcgtc gcccgcgctc ncgtacctct cgcgcgcac gcgcgtcctg tactcgttcg 2040
tccgcgagga gctcggcgtc aagggccgcc gcggcgacgt cttcctcggc aagcaggagg 2100
tgacgatcgg caccaacgtc tccgcacatc acgaggccat caagnncggc ngcatcaacc 2160
acgtcctcgt caagatgctc gcntagnnnc ncnncnann ctcgcntnnn nncnncnc 2220
nnncnncnnn nncntntng nntcgnntc ntgnncnnnn cgganntnnc nncnnnnnnn 2280
tnnnncntnn ctntctcnc nnnancnngt cnntnnnnnc tnnngntnn nnnncnnc 2340
ngtnnncann ncnctntnn nnnanncngg nanngantnn angntnncgn gnnncnnnnn 2400
nnnanaaann nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 2460
nnnnnnnnnn nnnnn 2475

<210> 21

<211> 726

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (12)..(719)

<223> "Xaa" means any amino acid; "Xaa" means no consensus at that position

<223> Description of Artificial Sequence: Consensus of
SEQ ID NOs: 13, 17, and 19

<400> 21

Met Ala Pro Ser Leu Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1 5 10 15

Xaa Asn Gly Xaa His Ala Ala Xaa Xaa Ala Ser Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Ala Xaa Ala Gly Ser Xaa Leu Pro Thr Thr Xaa Xaa
35 40 45

Thr Gln Leu Asp Ile Val Glu Xaa Xaa Leu Ala Asp Pro Xaa Thr Asp
50 55 60

Asp Xaa Xaa Glu Leu Asp Gly Tyr Ser Leu Thr Leu Gly Asp Val Val
65 70 75 80

Gly Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Xaa Asp Ser Asp Glu
85 90 95

Ile Arg Xaa Lys Ile Asp Lys Ser Val Glu Phe Leu Arg Xaa Gln Leu
100 105 110

Xaa Asn Ser Val Tyr Gly Val Thr Thr Gly Phe Gly Gly Ser Ala Asp
115 120 125

Thr Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His
130 135 140

Gln Leu Cys Gly Val Leu Pro Thr Ser Xaa Asp Ser Phe Xaa Leu Gly
145 150 155 160

Arg Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met
165 170 175

Thr	Ile	Arg	Val	Asn	Ser	Leu	Thr	Arg	Gly	His	Ser	Ala	Val	Arg	Leu	180	185	190
Val	Val	Leu	Glu	Ala	Leu	Thr	Asn	Phe	Leu	Asn	His	Gly	Ile	Thr	Pro	195	200	205
Ile	Val	Pro	Leu	Arg	Gly	Thr	Ile	Ser	Ala	Ser	Gly	Asp	Leu	Ser	Pro	210	215	220
Leu	Ser	Tyr	Ile	Ala	Ala	Ala	Ile	Thr	Gly	His	Pro	Asp	Ser	Lys	Val	225	230	235
His	Val	Xaa	His	Glu	Gly	Xaa	Glu	Lys	Ile	Met	Xaa	Ala	Arg	Glu	Ala	245	250	255
Ile	Ala	Leu	Phe	Gly	Leu	Glu	Pro	Val	Val	Leu	Gly	Pro	Lys	Glu	Gly	260	265	270
Leu	Gly	Leu	Val	Asn	Gly	Thr	Ala	Val	Ser	Ala	Ser	Met	Ala	Thr	Leu	275	280	285
Ala	Leu	His	Asp	Ala	His	Met	Leu	Ser	Leu	Leu	Ser	Gln	Ala	Leu	Thr	290	295	300
Ala	Leu	Thr	Val	Glu	Ala	Met	Val	Gly	His	Ala	Gly	Ser	Phe	His	Pro	305	310	315
Phe	Leu	His	Asp	Val	Thr	Arg	Pro	His	Pro	Thr	Gln	Ile	Glu	Val	Ala	325	330	335
Arg	Asn	Ile	Arg	Thr	Leu	Leu	Glu	Gly	Ser	Xaa	Phe	Ala	Val	His	His	340	345	350
Glu	Glu	Glu	Val	Lys	Val	Lys	Asp	Asp	Glu	Gly	Ile	Leu	Arg	Gln	Asp	355	360	365
Arg	Tyr	Pro	Leu	Arg	Thr	Ser	Pro	Gln	Trp	Leu	Gly	Pro	Leu	Val	Ser	370	375	380
Asp	Met	Ile	His	Ala	His	Ala	Val	Leu	Ser	Leu	Glu	Ala	Gly	Gln	Ser	385	390	395
																		400

Thr Thr Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His	405	410	415
Gly Gly Asn Phe Gln Ala Ser Ala Val Xaa Asn Thr Met Glu Lys Thr	420	425	430
Arg Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr	435	440	445
Glu Met Leu Asn Ala Gly Met Asn Arg Gly Leu Pro Ser Cys Leu Ala	450	455	460
Ala Glu Asp Pro Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala	465	470	475
Ala Ala Ala Tyr Thr Ser Glu Leu Gly His Leu Ala Asn Pro Val Thr	485	490	495
Thr His Val Gln Pro Ala Glu Met Gly Asn Gln Ala Val Asn Ser Leu	500	505	510
Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala Asn Asp Val Leu Ser	515	520	525
Leu Leu Leu Ala Thr His Leu Tyr Cys Val Leu Gln Ala Val Asp Leu	530	535	540
Arg Ala Met Glu Phe Glu Phe Lys Lys Gln Phe Xaa Pro Xaa Xaa Xaa	545	550	555
Xaa Leu Leu Xaa Gln His Phe Gly Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa	565	570	575
Xaa Xaa Glu Leu Xaa Xaa Lys Val Xaa Lys Xaa Leu Xaa Lys Arg Leu	580	585	590
Glu Gln Thr Asn Ser Tyr Asp Leu Glu Pro Arg Trp His Asp Ala Phe	595	600	605
Ser Xaa Ala Thr Gly Thr Val Val Glu Xaa Leu Ser Ser Xaa Xaa Xaa	610	615	620

Xaa Xaa Val Ser Leu Ala Ala Val Asn Ala Trp Lys Val Ala Xaa Ala
625 630 635 640

Glu Lys Ala Ile Ser Leu Thr Arg Xaa Val Arg Xaa Xaa Phe Trp Xaa
 645 650 655

Ala Pro Ser Ser Ser Ser Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr
 660 665 670

Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val Lys Ala Arg
 675 680 685

Arg Gly Asp Val Phe Leu Gly Lys Gln Glu Val Thr Ile Gly Ser Asn
 690 695 700

Val Ser Arg Ile Tyr Glu Ala Ile Lys Ser Gly Arg Ile Asn Xaa Val
705 710 715 720

Leu Val Lys Met Leu Ala
 725

<210> 22

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 74

<400> 22

atccatatgg ctctttcttt ggattctctt gctactacgc tcgccaacgg ctttacc 57

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 75

<400> 23

atcgcgggccg catgcggatc ctcattacgc gagcatcttg acgaggacgt gggtgatgcg 60

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 105

<400> 24

agtgaattca tggccccttc cttggactcg ctgcga

37

<210> 25

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer OLI 80

<400> 25

atcgcatgct cattacgcga gcatcttgac gaggacgtgg ttgatgcg

48

<210> 26

<211> 39

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: oli 89

<400> 26

taaaagatct ccaccatggc cccttccttg gactcgctc
39

<210> 27

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: oli 90

<400> 27

caagcggccg cagagacgcg ggatacgaaa gaactg
36

<210> 28

<211> 2741

<212> DNA

<213> Rhodotorula graminis

<220>

<221> modified_base

<222> (6)

<223> Description of modified_base: m = a or c

<220>

<221> exon

<222> (2008) .. (2586)

<223>

<220>

<221> exon

<222> (1822) .. (1947)

<223>

<220>

<221> exon

<222> (1587) .. (1748)

<223>

<220>

<221> exon

<222> (1365)..(1529)

<223>

<220>

<221> exon

<222> (961)..(1295)

<223>

<220>

<221> exon

<222> (449)..(880)

<223>

<220>

<221> exon

<222> (1)..(361)

<223>

<220>

<221> terminator

<222> (2587)..(2589)

<223>

<220>

<221> Intron

<222> (1948)..(2007)

<223>

<220>

<221> Intron

<223>

<221> Intron

<223>

<221> Intron

<223>

<221> Intron

<223>

<221> Intron

<223>

atg gcm cct tcc ttg gac tcg ctc gcc acc acg ctc gcc aac ggc ttt 48
Met Ala Pro Ser Leu Asp Ser Leu Ala Thr Thr Leu Ala Asn Gly Phe
1 5 10 15

acc aac ggc tgc cac gcc gct ccg acc aag tgc gct gcg ggc ccc act 96
Thr Asn Gly Ser His Ala Ala Pro Thr Lys Ser Ala Ala Gly Pro Thr
20 25 30

tcg gct ctc cgc cgc acg ccc ggc ctc gat ggc cac gcc gcg cac cag	144
Ser Ala Leu Arg Arg Thr Pro Gly Leu Asp Gly His Ala Ala His Gln	
35 40 45	
tcg cag ctc gag atc gtg cag gag ctc ctc agc gac ccc acc gac gac	192
Ser Gln Leu Glu Ile Val Gln Glu Leu Leu Ser Asp Pro Thr Asp Asp	
50 55 60	
gtc gtc gag ctc agc ggg tac agc ctc acc gtc cgt gac gtt gtc ggc	240
Val Val Glu Leu Ser Gly Tyr Ser Leu Thr Val Arg Asp Val Val Gly	
65 70 75 80	
gcc gcc cgc aag ggg cgc agg gtc cgc gtc cag aac gac gac gag atc	288
Ala Ala Arg Lys Gly Arg Arg Val Arg Val Gln Asn Asp Asp Glu Ile	
85 90 95	
cgc gca cgc gtc gac aag agc gtc gac ttc ctc aag gcc cag ctt cag	336
Arg Ala Arg Val Asp Lys Ser Val Asp Phe Leu Lys Ala Gln Leu Gln	
100 105 110	
aac tcg gtc tac gga gtc acc acg g tgcgttccga gacgagaggc	381
Asn Ser Val Tyr Gly Val Thr Thr	
115 120	
ggaaatctcg ggatgccgca gcgctgaacg ctgacactcg cttggacggc tgccgcggtc	441
ttgcagg gt ttc ggt ggc tcg gcc gac acg agg act gag gat gca gtc	489
Gly Phe Gly Gly Ser Ala Asp Thr Arg Thr Glu Asp Ala Val	
125 130	
agc ctc cag aag gcg ctc atc gag cac cag ctc tgc ggc gtg acg ccg	537
Ser Leu Gln Lys Ala Leu Ile Glu His Gln Leu Cys Gly Val Thr Pro	
135 140 145 150	

acg tcc gtc tgc tcc ttc agc gtc gga cgc ggc ctc gag aac acg ctt	585
Thr Ser Val Ser Ser Phe Ser Val Gly Arg Gly Leu Glu Asn Thr Leu	
155 160 165	
ccg ctc gag gtc gtc cgc ggc gcc atg gtc atc cgc gtc aac tgc ctc	633
Pro Leu Glu Val Val Arg Gly Ala Met Val Ile Arg Val Asn Ser Leu	
170 175 180	
acg cgt ggc cac tgc gcc gtc cgc ctc gtc gtc ctt gag gcg ctc acc	681
Thr Arg Gly His Ser Ala Val Arg Leu Val Val Leu Glu Ala Leu Thr	
185 190 195	
aac ttc ttg aac cac cgc atc acg ccc atc gtc ccc ctc cgc ggc tcc	729
Asn Phe Leu Asn His Arg Ile Thr Pro Ile Val Pro Leu Arg Gly Ser	
200 205 210	
atc tgc gcg tgc ggc gac ctc agc ccg ctc tgc tac atc gcc ggc gcc	777
Ile Ser Ala Ser Gly Asp Leu Ser Pro Leu Ser Tyr Ile Ala Gly Ala	
215 220 225 230	
atc acc ggt cac ccc gac gtc aag gtt cac gtt ttg cac gag gga acc	825
Ile Thr Gly His Pro Asp Val Lys Val His Val Leu His Glu Gly Thr	
235 240 245	
gag aag atc atg ttt gcg cgc gag gcc atc tgc ctc ttt ggt ctc gag	873
Glu Lys Ile Met Phe Ala Arg Glu Ala Ile Ser Leu Phe Gly Leu Glu	
250 255 260	
gca gtc g gtacgtcgcg agtcctgact gcagtgagct gttcgagagt ctcccagttt	930
Ala Val	

gctgactgcc ctttgttcat gcgattgcag tc ctc ggc ccg aag gag ggt ctc 983
Val Leu Gly Pro Lys Glu Gly Leu
270

ggt ctg gtc aac gga acg gcc gtc tcc gcc tcg atg gcg acc ctc agt 1031
Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ser
275 280 285

ctg cac gac tcg cac atg ctc tcg ctc ctc tcg cag gcc ttg acg gct 1079
Leu His Asp Ser His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
290 295 300

ctc acg gtg gag gcc atg gtc ggc cag cag ggc tcg ttc gcg ccg ttc 1127
Leu Thr Val Glu Ala Met Val Gly Gln Gln Gly Ser Phe Ala Pro Phe
305 310 315 320

atc cac gac gtc tgc cgc ccg cac ccc ggc cag gtc gag gtc gcg cgc 1175
Ile His Asp Val Cys Arg Pro His Pro Gly Gln Val Glu Val Ala Arg
325 330 335

aac atc cgc acg ctc ctt tcc ggc tcg tcg ttt gcc gtt gag cac gag 1223
Asn Ile Arg Thr Leu Leu Ser Gly Ser Ser Phe Ala Val Glu His Glu
340 345 350

gag gag gtc aag gtc aag gac gac gag ggc att ctt cgc cag gac cgc 1271
Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
355 360 365

tac ccg ctc cgc acg tcg cct cag gttcgtcccc tctctctccc ctccctccg 1325
Tyr Pro Leu Arg Thr Ser Pro Gln
370 375

tccgaccggc gcgtegagac ttacgttttg cgtatccag ttc ctc ggc ccg ctc	1379
Phe Leu Gly Pro Leu	
380	
gtg gag gac atg atg cac gcc tac tcg act ctc tcg ctc gag aac aac	1427
Val Glu Asp Met Met His Ala Tyr Ser Thr Leu Ser Leu Glu Asn Asn	
385 390 395	
acg acg acc gac aac ccg ctc ctc gac gtc gag aac aag cag acc gcg	1475
Thr Thr Thr Asp Asn Pro Leu Leu Asp Val Glu Asn Lys Gln Thr Ala	
400 405 410	
cac ggc ggc aac ttc cag gcg tcg gct gtc tcg att tcg atg gag aag	1523
His Gly Gly Asn Phe Gln Ala Ser Ala Val Ser Ile Ser Met Glu Lys	
415 420 425	
acc agg tgcgtctctc gctgccttcg tactccgata ttgtgctgaa tggtcttctc	1579
Thr Arg	
430	
ctgcagg ctc gca ctc gcc ctc atc ggc aag ctc aac ttc acg cag tgc	1628
Leu Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Cys	
435 440 445	
acc gag ttg ctc aac gct gcc atg aac cgc ggc ctg cct tcg tgc ctc	1676
Thr Glu Leu Leu Asn Ala Ala Met Asn Arg Gly Leu Pro Ser Cys Leu	
450 455 460	
gct gcc gag gac ccg tcg ctc aac tat cac ggc aag ggc ttg gac att	1724
Ala Ala Glu Asp Pro Ser Leu Asn Tyr His Gly Lys Gly Leu Asp Ile	
465 470 475	

cac atc gct gct tac gct tcg gag gtgagccgtc gacgtttctcc gccgctcgtc 1778
 His Ile Ala Ala Tyr Ala Ser Glu

480

485

gtcccccttca ggcaccccag gctgacttcc ttccctctg tag ctc ggc cac ctt 1833
 Leu Gly His Leu

gcc aac ccg gtc act acc ttc gtc cag ccc gca gag atg ggc aac cag 1881
 Ala Asn Pro Val Thr Thr Phe Val Gln Pro Ala Glu Met Gly Asn Gln

490

495

500

505

gcc gtc aac tcg ctc gct ctc atc tcc gcg cgc cgc act gcc gag gcc 1929
 Ala Val Asn Ser Leu Ala Leu Ile Ser Ala Arg Arg Thr Ala Glu Ala

510

515

520

aac gac gtc ctt tct ctc gtgcgttcgt gtgcgaatga gtcccgacgc 1977
 Asn Asp Val Leu Ser Leu

525

aatagcgact gactgcgcga tcctgagcag ctt ctc gcc tcg cac ctg tac tgc 2031
 Leu Leu Ala Ser His Leu Tyr Cys

530

535

acg ctc cag gcc gtc gac ctc cgc gcg atg gag ctc gac ttc aag aag 2079
 Thr Leu Gln Ala Val Asp Leu Arg Ala Met Glu Leu Asp Phe Lys Lys

540

545

550

cag ttc gac ccg ctt ctc ccg act ctc ctc cag cag cac ctc ggc act 2127
 Gln Phe Asp Pro Leu Leu Pro Thr Leu Leu Gln Gln His Leu Gly Thr

555

560

565

ggc ctc gac gtc aac gca ctt gcg ctc gag gtc aag aag gcg ctc aac	2175
Gly Leu Asp Val Asn Ala Leu Ala Leu Glu Val Lys Lys Ala Leu Asn	
570 575 580	
aag cgt ctc gag cag acg acg acg tac gac ctc gag ccg cgc tgg cac	2223
Lys Arg Leu Glu Gln Thr Thr Thr Tyr Asp Leu Glu Pro Arg Trp His	
585 590 595	
gac gcc ttc tcg tac gcg acc ggc acc gtc gtc gag ctc ctc tcg tcc	2271
Asp Ala Phe Ser Tyr Ala Thr Gly Thr Val Val Glu Leu Leu Ser Ser	
600 605 610 615	
tcg ccc tct gcc aac gtc acc ctt act gcc gtc aac gcg tgg aag gtt	2319
Ser Pro Ser Ala Asn Val Thr Leu Thr Ala Val Asn Ala Trp Lys Val	
620 625 630	
gcc tcg gcc gag aag gcc atc tcg ctc acg cgc gag gtg cgc aac cgc	2367
Ala Ser Ala Glu Lys Ala Ile Ser Leu Thr Arg Glu Val Arg Asn Arg	
635 640 645	
ttc tgg cag acg ccg tct tcg cag gcg ccg gcg cac gca tac ctc tcg	2415
Phe Trp Gln Thr Pro Ser Ser Gln Ala Pro Ala His Ala Tyr Leu Ser	
650 655 660	
ccg cgc acg cgc gtc ctg tac tcg ttc gtg cgc gag gag ctc ggc gtg	2463
Pro Arg Thr Arg Val Leu Tyr Ser Phe Val Arg Glu Glu Leu Gly Val	
665 670 675	
cag gcg cgc cgc ggc gac gtg ttt gtc ggc gtg cag cag gag acg atc	2511
Gln Ala Arg Arg Gly Asp Val Phe Val Gly Val Gln Gln Glu Thr Ile	
680 685 690 695	

ggg agc aac gtc tcg cgc atc tac gag gcc atc aag gac ggc cgc atc 2559
 Gly Ser Asn Val Ser Arg Ile Tyr Glu Ala Ile Lys Asp Gly Arg Ile
 700 705 710

aac cac gtc ctc gtc aag atg ctc gcg taaggcccgga gcaagcctcg 2606
 Asn His Val Leu Val Lys Met Leu Ala
 715 720

cctagacgcc cgcctcaccc caagaccagc ttttcgacgt cgtgtcgtgc caagaacgga 2666

ctttcctcca tacacatgtc gtcttactct ctcgccgtca tcacgtctct cagttctttc 2726

gtatcccgcg tctct 2741

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 <213> Artificial Sequence

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 theoretical sequence based in part on SEQ ID NO:20

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 <222> (1)..(2163)
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<400> 29
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 Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
 1 5 10 15

dca aac ggv thg cac gcc gct ccg hcc aag ycg scw acg ggc gcc acg 96
 Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr
 20 25 30

tcc ach ctc mgm cgg ccg bcc dgg ctc gct cct ccc gcc acc cag vhg 144
 Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa
 35 40 45

acg cag ctc gac atc gtb gag vag atc ctc gcc gac ccc acc gac gac	192
Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp	
50 55 60	
gws vtc gaa ctc gac ggg tac acc ctc acc ctc ggh gac gtc gtc ggc	240
Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly	
65 70 75 80	
gcc gcb cgc aag ggc cgc hcb gtc cgc gtc cag aca gmc gac gag atc	288
Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile	
85 90 95	
cgc gca aag atc gac aav agb gtc gag ttc ctc cgb dcb cag ctc bac	336
Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa	
100 105 110	
aac agb gtc tac ggh gtc acg act ggt ttc ggc ggc tcg gcc gac acc	384
Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr	
115 120 125	
cgg act gag gat gcv atc tcg ctc cag aag gcb ctc ctc gag cac cag	432
Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln	
130 135 140	
ctc tgc ggt gtb ctc ccb acg tcg dtc gab tcc ttc vgc ctc ggh cgc	480
Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg	
145 150 155 160	
ggc ctc gag aac tcg ctt ccg ctc gag gtc gtc cgc ggc gcc atg acc	528
Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr	
165 170 175	
atc cgc gtc aac tcg ctc acb cgc ggc cac tcg gcb gtc cgc ctc gtc	576
Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val	
180 185 190	
gtc ctc gag gcg ctc acc aac ttc ctc aac cac ggc atc acc ccc atc	624
Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile	
195 200 205	
gtc ccc ctc cgc ggc acc atc tcg gcg tcg ggc gac ctc tcc ccb ctc	672
Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu	
210 215 220	
tcb tac atc gcc gcc gcc atc acc ggt cac ccg gac dbc aag gtb cac	720
Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His	
225 230 235 240	
gty kts cac gag ggc ams gag aag atc atg thc gcc cgc gag gcg atc	768
Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile	
245 250 255	

gcg ctc ttb ggt ctc gag ccc gtc gtc ctc ggc ccg aag gag ggt ctc Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu 260 265 270	816
ggt ctc gtc aac ggc acg gcc gtc tcc gcc tcg atg gcg acc ctc gct Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala 275 280 285	864
ctg cac gac gca cac atg ctc tcg ctc ctc tcg cag gcg ctc acg gct Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala 290 295 300	912
ctb acg gtc gag gcc atg gtc ggc cac gcc ggc tcg ttc cac ccv ttc Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe 305 310 315 320	960
ctc cac gac gtc acg cgc cct cac ccg acc cag atc gag gtc gcg cgc Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg 325 330 335	1008
aac atc cgc acg ctc ctc gag ggc agc hvg ttt gcc gtc cac cac gag Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu 340 345 350	1056
gag gag gtc aag gtc aag gac gac gag ggc att ctc cgc cag gac cgc Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg 355 360 365	1104
tac ccg ctc cgc acg tcg cct cag tgg ctc ggc ccg ctc gtc agc gac Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp 370 375 380	1152
atg att cac gcc cac gcb gtc ctc tcg ctc gag gcc gag tcg acg acc Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr 385 390 395 400	1200
gac aac ccg ctc atc gac gtc gag aac aag ahg acc cac cac ggc ggc Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly 405 410 415	1248
aac ttc cag gcg dcc gct gtc gcv aac acg atg gag aag act cgc ctc Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu 420 425 430	1296
gcv ctc gcc ctg atc ggc aag ctc aac ttc acg cag ctc acc gag atg Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met 435 440 445	1344
ctc aac gcc ggc atg aac cgc ggc ctb ccb tcc tgc ctc gct gcc gag Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu 450 455 460	1392

gac ccb tcg ctc tcc tat cac tgc aag ggc ctc gac att gcc gcb gcb Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala 465 470 475 480	1440
gcb tac act tcg gag ctc ggh cac ctt gcc aac ccg gtb acg acc cac Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His 485 490 495	1488
gtc cag ccg gch gag atg ggc aac cag gcc gtc aac tcg ctc gcb ctc Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu 500 505 510	1536
atc tcg gcb cgc cgc acb gcc gag gcc aac gac gtc ctt tct ctc ctc Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu 515 520 525	1584
ctc gcc acc cac ctc tac tgc gtb ctc cag gcc gtc gac ctc cgc gcg Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala 530 535 540	1632
atg gag ttc gag ttc aag aag cag ttc gac ccg vtb vtc vcb dcg ctc Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu 545 550 555 560	1680
htc vag cag cac ttt ggc dcg gcc ctc gac ggc wac gaa ctc ghg gac Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp 565 570 575	1728
aag gtc aac aag dcg ctc dac aag cgb ctc gag cag acc aac tcg tac Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr 580 585 590	1776
gac ctc gag ccg cgc tgg cac gac gcc ttc tcg ttc gcg acc ggc acc Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr 595 600 605	1824
gtc gtc gag ctc ctc tcg tcc tcg ccb yct gcc aag gtc tcg ctc gcb Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala 610 615 620	1872
gcc gtc aac gcc tgg aag gtc gcc tcc gcc gag aag gcc atc tcg ctc Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu 625 630 635 640	1920
acg cgc bav gtc cgc gac hcc ttc tgg bcc gcb ccg tcg tcg tcg tcg Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser 645 650 655	1968
ccc gcg ctc dcg tac ctc tcg ccg cgc acg cgc gtc ctg tac tcg ttc Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe 660 665 670	2016

gtc cgc gag gag ctc ggc gtc aag gcc cgc cgc ggc gac gtc ttc ctc	2064
Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu	
675 680 685	
ggc aag cag gag gtg acg atc ggc acc aac gtc tcc cgc atc tac gag	2112
Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu	
690 695 700	
gcc atc aag dvc ggc hgc atc aac cac gtc ctc gtc aag atg ctc gcd	2160
Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala	
705 710 715 720	
tag	2163

<210> 30
 <211> 720
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<220>
 <223> Description of Artificial Sequence: Preferred
 theoretical sequence based in part on SEQ ID NO:20

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 <222> (5)..(5)
 <223> The 'Xaa' at location 5 stands for Val, Leu, or Phe.

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> The 'Xaa' at location 12 stands for Val, Leu, or Phe.

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> The 'Xaa' at location 16 stands for Val, Leu, or Phe.

<220>
 <221> misc_feature
 <222> (17)..(17)
 <223> The 'Xaa' at location 17 stands for Thr, Ala, or Ser.

<220>
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 <222> (19)..(19)
 <223> The 'Xaa' at location 19 stands for Gly.

<220>
 <221> misc_feature
 <222> (20)..(20)
 <223> The 'Xaa' at location 20 stands for a stop codon, Ser, or Leu.

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> The 'Xaa' at location 25 stands for Thr, Pro, or Ser.

<220>
 <221> misc_feature
 <222> (27)..(27)
 <223> The 'Xaa' at location 27 stands for Pro, or Ser.

<220>
 <221> misc_feature
 <222> (28)..(28)
 <223> The 'Xaa' at location 28 stands for Ala, or Pro.

<220>
 <221> misc_feature
 <222> (34)..(34)
 <223> The 'Xaa' at location 34 stands for Thr.

<220>
 <221> misc_feature
 <222> (36)..(36)
 <223> The 'Xaa' at location 36 stands for Arg, or Ser.

<220>
 <221> misc_feature
 <222> (39)..(39)
 <223> The 'Xaa' at location 39 stands for Ala, Pro, or Ser.

<220>
 <221> misc_feature
 <222> (40)..(40)
 <223> The 'Xaa' at location 40 stands for Arg, Gly, or Trp.

<220>
 <221> misc_feature
 <222> (48)..(48)
 <223> The 'Xaa' at location 48 stands for Lys, Thr, Met, Glu, Ala, Val, Gln, Pro, or Leu.

<220>
 <221> misc_feature
 <222> (54)..(54)
 <223> The 'Xaa' at location 54 stands for Val.

<220>
 <221> misc_feature
 <222> (56)..(56)
 <223> The 'Xaa' at location 56 stands for Lys, Glu, or Gln.

<220>
 <221> misc_feature
 <222> (65)..(65)
 <223> The 'Xaa' at location 65 stands for Glu, Asp, or Val.

<220>
 <221> misc_feature
 <222> (66)..(66)
 <223> The 'Xaa' at location 66 stands for Ile, Val, or Leu.

<220>
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 <223> The 'Xaa' at location 76 stands for Gly.

<220>
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 <222> (87)..(87)
 <223> The 'Xaa' at location 87 stands for Thr, Pro, or Ser.

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 <222> (93)..(93)
 <223> The 'Xaa' at location 93 stands for Asp, or Ala.

<220>
 <221> misc_feature
 <222> (102)..(102)
 <223> The 'Xaa' at location 102 stands for Lys, or Asn.

<220>
 <221> misc_feature
 <222> (103)..(103)
 <223> The 'Xaa' at location 103 stands for Arg, or Ser.

<220>
 <221> misc_feature
 <222> (109)..(109)
 <223> The 'Xaa' at location 109 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (112)..(112)
 <223> The 'Xaa' at location 112 stands for Asp, His, or Tyr.

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<221> misc_feature
<222> (114)..(114)
<223> The 'Xaa' at location 114 stands for Arg, or Ser.

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<221> misc_feature
<222> (117)..(117)
<223> The 'Xaa' at location 117 stands for Gly.

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<222> (148)..(148)
<223> The 'Xaa' at location 148 stands for Val.

<220>
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<222> (150)..(150)
<223> The 'Xaa' at location 150 stands for Pro.

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<222> (153)..(153)
<223> The 'Xaa' at location 153 stands for Ile, Val, or Phe.

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<222> (154)..(154)
<223> The 'Xaa' at location 154 stands for Glu, or Asp.

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<221> misc_feature
<222> (157)..(157)
<223> The 'Xaa' at location 157 stands for Ser, Gly, or Arg.

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<222> (159)..(159)
<223> The 'Xaa' at location 159 stands for Gly.

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<223> The 'Xaa' at location 183 stands for Thr.

<220>
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<222> (223)..(223)
<223> The 'Xaa' at location 223 stands for Pro.

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<221> misc_feature
<222> (225)..(225)
<223> The 'Xaa' at location 225 stands for Ser.

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<221> misc_feature
<222> (237)..(237)
<223> The 'Xaa' at location 237 stands for Ser, Thr, Ile, Gly, Ala,
Val,
      Cys, or Phe.

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<221> misc_feature
<222> (239)..(239)
<223> The 'Xaa' at location 239 stands for Val.

<220>
<221> misc_feature
<222> (241)..(241)
<223> The 'Xaa' at location 241 stands for Val.

<220>
<221> misc_feature
<222> (242)..(242)
<223> The 'Xaa' at location 242 stands for Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (246)..(246)
<223> The 'Xaa' at location 246 stands for Lys, Asn, or Thr.

<220>
<221> misc_feature
<222> (251)..(251)
<223> The 'Xaa' at location 251 stands for Tyr, Ser, or Phe.

<220>
<221> misc_feature
<222> (259)..(259)
<223> The 'Xaa' at location 259 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (305)..(305)
<223> The 'Xaa' at location 305 stands for Leu.

<220>
<221> misc_feature

<222> (319)..(319)
<223> The 'Xaa' at location 319 stands for Pro.

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<220>
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 <222> (346)..(346)
 <223> The 'Xaa' at location 346 stands for Lys, Arg, Thr, Gln, Pro, a
 stop codon, Trp, or Ser.

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 <221> misc_feature
 <222> (411)..(411)
 <223> The 'Xaa' at location 411 stands for Lys, Thr, or Met.

<220>
 <221> misc_feature
 <222> (421)..(421)
 <223> The 'Xaa' at location 421 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (457)..(457)
 <223> The 'Xaa' at location 457 stands for Leu.

<220>
 <221> misc_feature
 <222> (458)..(458)
 <223> The 'Xaa' at location 458 stands for Pro.

<220>
 <221> misc_feature
 <222> (466)..(466)
 <223> The 'Xaa' at location 466 stands for Pro.

<220>
 <221> misc_feature
 <222> (487)..(487)
 <223> The 'Xaa' at location 487 stands for Gly.

<220>
 <221> misc_feature
 <222> (493)..(493)
 <223> The 'Xaa' at location 493 stands for Val.

<220>
 <221> misc_feature
 <222> (518)..(518)
 <223> The 'Xaa' at location 518 stands for Thr.

<220>
 <221> misc_feature
 <222> (536)..(536)
 <223> The 'Xaa' at location 536 stands for Val.

<220>
 <221> misc_feature
 <222> (556)..(556)
 <223> The 'Xaa' at location 556 stands for Met, Ile, Val, or Leu.

<220>
 <221> misc_feature
 <222> (557)..(557)
 <223> The 'Xaa' at location 557 stands for Ile, Val, or Leu.

<220>
 <221> misc_feature
 <222> (558)..(558)
 <223> The 'Xaa' at location 558 stands for Thr, Ala, or Pro.

<220>
 <221> misc_feature
 <222> (559)..(559)
 <223> The 'Xaa' at location 559 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (561)..(561)
 <223> The 'Xaa' at location 561 stands for Ile, Leu, or Phe.

<220>
 <221> misc_feature
 <222> (562)..(562)
 <223> The 'Xaa' at location 562 stands for Lys, Glu, or Gln.

<220>
 <221> misc_feature
 <222> (567)..(567)
 <223> The 'Xaa' at location 567 stands for Thr, Ala, or Ser.

<220>
 <221> misc_feature
 <222> (572)..(572)
 <223> The 'Xaa' at location 572 stands for Asn, or Tyr.

<220>
 <221> misc_feature
 <222> (575)..(575)
 <223> The 'Xaa' at location 575 stands for Glu, Ala, or Val.

<220>
 <221> misc_feature
 <222> (581)..(581)
 <223> The 'Xaa' at location 581 stands for Thr, Ala, or Ser.

<220>

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<221> misc_feature
<222> (583)..(583)
<223> The 'Xaa' at location 583 stands for Asn, Asp, or Tyr.

<220>
<221> misc_feature
<222> (617)..(617)
<223> The 'Xaa' at location 617 stands for Pro.

<220>
<221> misc_feature
<222> (618)..(618)
<223> The 'Xaa' at location 618 stands for Pro, or Ser.

<220>
<221> misc_feature
<222> (643)..(643)
<223> The 'Xaa' at location 643 stands for Glu, Asp, Gln, His, a stop
      codon, or Tyr.

<220>
<221> misc_feature
<222> (647)..(647)
<223> The 'Xaa' at location 647 stands for Thr, Pro, or Ser.

<220>
<221> misc_feature
<222> (650)..(650)
<223> The 'Xaa' at location 650 stands for Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> (660)..(660)
<223> The 'Xaa' at location 660 stands for Thr, Ala, or Ser.

<220>
<221> misc_feature
<222> (708)..(708)
<223> The 'Xaa' at location 708 stands for Asn, Ser, Thr, Asp, Gly,
      Ala, Tyr, or Cys.

<220>
<221> misc_feature
<222> (710)..(710)
<223> The 'Xaa' at location 710 stands for Ser, Arg, or Cys.

<400> 30
Met Ala Pro Ser Xaa Asp Ser Ile Ala Thr Ser Xaa Ala Asn Gly Xaa
1          5          10          15

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Xaa Asn Xaa Xaa His Ala Ala Pro Xaa Lys Xaa Xaa Thr Gly Ala Thr	20	25	30
Ser Xaa Leu Xaa Arg Pro Xaa Xaa Leu Ala Pro Pro Ala Thr Gln Xaa	35	40	45
Thr Gln Leu Asp Ile Xaa Glu Xaa Ile Leu Ala Asp Pro Thr Asp Asp	50	55	60
Xaa Xaa Glu Leu Asp Gly Tyr Thr Leu Thr Leu Xaa Asp Val Val Gly	65	70	75
Ala Ala Arg Lys Gly Arg Xaa Val Arg Val Gln Thr Xaa Asp Glu Ile	85	90	95
Arg Ala Lys Ile Asp Xaa Xaa Val Glu Phe Leu Arg Xaa Gln Leu Xaa	100	105	110
Asn Xaa Val Tyr Xaa Val Thr Thr Gly Phe Gly Gly Ser Ala Asp Thr	115	120	125
Arg Thr Glu Asp Ala Ile Ser Leu Gln Lys Ala Leu Leu Glu His Gln	130	135	140
Leu Cys Gly Xaa Leu Xaa Thr Ser Xaa Xaa Ser Phe Xaa Leu Xaa Arg	145	150	155
Gly Leu Glu Asn Ser Leu Pro Leu Glu Val Val Arg Gly Ala Met Thr	165	170	175
Ile Arg Val Asn Ser Leu Xaa Arg Gly His Ser Ala Val Arg Leu Val	180	185	190
Val Leu Glu Ala Leu Thr Asn Phe Leu Asn His Gly Ile Thr Pro Ile	195	200	205
Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser Xaa Leu	210	215	220

Xaa Tyr Ile Ala Ala Ala Ile Thr Gly His Pro Asp Xaa Lys Xaa His
 225 230 235 240

Xaa Xaa His Glu Gly Xaa Glu Lys Ile Met Xaa Ala Arg Glu Ala Ile
 245 250 255

Ala Leu Xaa Gly Leu Glu Pro Val Val Leu Gly Pro Lys Glu Gly Leu
 260 265 270

Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ser Met Ala Thr Leu Ala
 275 280 285

Leu His Asp Ala His Met Leu Ser Leu Leu Ser Gln Ala Leu Thr Ala
 290 295 300

Xaa Thr Val Glu Ala Met Val Gly His Ala Gly Ser Phe His Xaa Phe
 305 310 315 320

Leu His Asp Val Thr Arg Pro His Pro Thr Gln Ile Glu Val Ala Arg
 325 330 335

Asn Ile Arg Thr Leu Leu Glu Gly Ser Xaa Phe Ala Val His His Glu
 340 345 350

Glu Glu Val Lys Val Lys Asp Asp Glu Gly Ile Leu Arg Gln Asp Arg
 355 360 365

Tyr Pro Leu Arg Thr Ser Pro Gln Trp Leu Gly Pro Leu Val Ser Asp
 370 375 380

Met Ile His Ala His Ala Val Leu Ser Leu Glu Ala Glu Ser Thr Thr
 385 390 395 400

Asp Asn Pro Leu Ile Asp Val Glu Asn Lys Xaa Thr His His Gly Gly
 405 410 415

Asn Phe Gln Ala Xaa Ala Val Ala Asn Thr Met Glu Lys Thr Arg Leu
 420 425 430

Ala Leu Ala Leu Ile Gly Lys Leu Asn Phe Thr Gln Leu Thr Glu Met
435 440 445

Leu Asn Ala Gly Met Asn Arg Gly Xaa Xaa Ser Cys Leu Ala Ala Glu
450 455 460

Asp Xaa Ser Leu Ser Tyr His Cys Lys Gly Leu Asp Ile Ala Ala Ala
465 470 475 480

Ala Tyr Thr Ser Glu Leu Xaa His Leu Ala Asn Pro Xaa Thr Thr His
485 490 495

Val Gln Pro Arg Glu Met Gly Asn Gln Ala Val Asn Ser Leu Ala Leu
500 505 510

Ile Ser Ala Arg Arg Xaa Ala Glu Ala Asn Asp Val Leu Ser Leu Leu
515 520 525

Leu Ala Thr His Leu Tyr Cys Xaa Leu Gln Ala Val Asp Leu Arg Ala
530 535 540

Met Glu Phe Glu Phe Lys Lys Gln Phe Asp Pro Xaa Xaa Xaa Xaa Leu
545 550 555 560

Xaa Xaa Gln His Phe Gly Xaa Ala Leu Asp Gly Xaa Glu Leu Xaa Asp
565 570 575

Lys Val Asn Lys Xaa Leu Xaa Lys Arg Leu Glu Gln Thr Asn Ser Tyr
580 585 590

Asp Leu Glu Pro Arg Trp His Asp Ala Phe Ser Phe Ala Thr Gly Thr
595 600 605

Val Val Glu Leu Leu Ser Ser Ser Xaa Xaa Ala Lys Val Ser Leu Ala
610 615 620

Ala Val Asn Ala Trp Lys Val Ala Ser Ala Glu Lys Ala Ile Ser Leu
625 630 635 640

Thr Arg Xaa Val Arg Asp Xaa Phe Trp Xaa Ala Pro Ser Ser Ser Ser
645 650 655

Pro Ala Leu Xaa Tyr Leu Ser Pro Arg Thr Arg Val Leu Tyr Ser Phe
660 665 670

Val Arg Glu Glu Leu Gly Val Lys Ala Arg Arg Gly Asp Val Phe Leu
675 680 685

Gly Lys Gln Glu Val Thr Ile Gly Thr Asn Val Ser Arg Ile Tyr Glu
690 695 700

Ala Ile Lys Xaa Gly Xaa Ile Asn His Val Leu Val Lys Met Leu Ala
705 710 715 720